

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCACGCCGCAGGACCTGGAGGTCCGGCTCGCTTCCCG
CAGCGCTACCCGCCATCGCCTGCCGCCGGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGACGCCCTGCCACCAGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACGAACTTGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA
GGCGACGGGTCTGCCGGTCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAACG
GAAGATGCCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACTGAATGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCACTCTAGAGTCGACCTGCAGAACG
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEP PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCGTCTAACCGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCGGAGGAGCGCCTTC
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCTGTGCGCTGGCACTGCGGCGGAGGC
CGGGCCGCCAGGAGGAGGCAGCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGCTCTGGCCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCCAGGCAGGTGCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCCCTGATGGGTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACTGTGACAAAGCAAACGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGTGGCACAT
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTTATTAGCT
TCATTATAAACTCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTAGTTGGCAGATATTCAAAATTACAATGCATTATGGT
TCAGGTTAAATTTCTGTTAGTTGGCAGATATTCAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAAGTATTAGAT
GTTTGTACATTTAAAAATTGCTCTAATTAAACTCTCAATACAATATATTGGACC
TTACCAATTCCAGAGATTCACTATTAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAATATAATGTATGAACTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTACCTAATAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCAAC TTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
```

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCTGGCGTCCGGGTGCAGAGCCAGGAGGCCGGAGGCAGCGCGCGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAACGAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGGACCTGTGCTGCCCGCGTGCACGACTGTGCCCTGCCAACCTGGCGCCATCT
GTTACTGTGACCTCTCTGCACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTGGAAACGTACTGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGGCATGCCCTGGATGAGGGCATTGCCTACGCCCTGGGACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCCGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAAATAACATGACATCTACCAAGGTAACCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAAGGAGCTGATGGAGAACGGCCCTGTCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAACCTCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCGCATCGTGCAGCGCTCAATGAGTGCACATCGAG
AGCTTGTGCTGGCGTCTGGGCGCTGGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
CGGGCACCACGCCGGGTCCGGCTGGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGGCAGGCCGGCTTAAT
CCCAGCGGGTTCCGCTGACGCAGGCCCGCTGGAGGCCGGCAGGCCGGAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGAGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGGCCCTGGGACTAACAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAAATCCGTATTCTTTTTTTTTAGACAGGGTCTTGTCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACACCTGGC
TAATTTTGATTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGCGGCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGATGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGTACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGGTGGAGCCTGTCCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCCCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFFHGPAGFSTLNPLVRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

T02ET20-E41E5060

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCACCGGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTCTGGAGAACAACTATACGCCTTCCAGAACGCCGGCACGAGG

GCTGGTTCATGGCCTTCACGCGGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGCAGTCAGTTGAGTTGTGGCTCCGCCACCCGCCGACCAAGGCCACAC
GGCGGCCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCACCTGATCTCAGGCCACCAGCCTGCGCCCTCCAGCCGGCTCCTGAAGCC

CGCTGAAAGGTCAGCGACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCCGGTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGGGAGGAAAGAAAGGGAGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTCAGTGTGGAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTGGATTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGCAAACCTCTGGCCTGCC
CTAGTGTGCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCTAACCGTACTCTACCTCCACAACAAACCAATTAAATAATGC
TGGATTTCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGCAGGAAAC
AATATTGAGACCATTTCACGGCTGCTTGCCCAGCTTGAAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTATTGTGGACGGAACCTCCTGACCAACAAAGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACAGAT
AAACACATTCTTGACAGCCTCTCAAATCTGCTAACGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCTGGTTTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTCATCTCTAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTAGGGAATTAAATATGAATCTTGTCCCTGCCCACCACGACCCCCGGCCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTTCTCGACCCTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAAGCTACACGCCTCCAACCTCCTACCACATGAAACTTCCCACGATT
CTGACTGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGATA
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTTAGAGGC
CACCAACCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAAGTGGAAATACAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTCACTCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTTCAACTGCAGCCATTACACCCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGACAATTAGACTCTTGAGAA
CACACTCGTGTGACATAAAAGACACCGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTCATTGAATACTCTGTAATTACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAAATTACAAACAGTTGTAACCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRNFVYCNERSLTSVPLGIP~~
EGVT~~VLYLHNNQINNAGFPaelHNvQSVHTVYLYGNQLDEFPMNLPKNRVLHLQENNIQTI~~
SRAALAQLLKLEELH~~DDNSISTVGVEDGAFREAI~~SLKLLFLSKNHLS~~SSVPVGLPVDLQELR~~
VDENRIAVISDMAFQNL~~TSLERLIVDGNLLTNKGIAEGTFSHLT~~KLKEFSIVRN~~NLSHPPPDLPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNL~~SNLKQLTARNN
PWFCDCS~~I~~KWVTEWLKYIPSSLNVRG~~FMCQGPEQVRGM~~AVRELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTSKLPTIPDWDGRERVT~~PP~~PISERIQLSIHFVND
TSIQVSWL~~SLSFTVMAYKLTWVKGHS~~LVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVE~~DTICSEATTHASYLNN~~GNTASHEQTTSHSMGSPFLLAGLIGGA~~VIFV~~L~~V~~V~~L~~
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKD~~NSILEMTETSFQIV~~SLNN~~DQL~~LKG
DFRLQPIYTPNGGINYTDCHI~~PNNMRYCNS~~VPDLEH~~CHT~~

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTGGAGCAAGCGCGGCGGAGACAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCCACGAGCG
ATCCCGAGGAAGAGCGCGGCCCTCGCGAGGCAGAGGCCAGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCCAGGCAGCGGCCCTCGCAGCCTGCCCCCTCTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGACAGATCGTCTCCTCCCTGCCAGGGCAGGGAGCGGTACAGTGGGAGGTCCATCT
CTAGGGCAGACACGCTCGAACCCACCGCAGACGGCCCTCTGGAGAGTCTGTGAGAACACAAGGGCAGACC
TGGTTTCATCATGACAGCTCTCGCAGTGTCAAACACCATGACTATGCAAAGGTCAAGGGAGTTCATCGTGGACA
CTCTGCAATTCTGGACATTGGTCTCTGATGTCAACCGAGTGGGCTGCTCAAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGAGCGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGTCATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGTA
AGGACGGGACACGGGCATCTAACATTGGCATTGGTGTGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGGCCACATGTGCAGCACCTGGAGCATACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCAAGTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCTCTGAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTGAAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCAAATGGAAAACCTGCAGCCAGTGGACCAACTGTGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCTCGTGTGCAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGACCACGGTTGTGAACATTCTGTGTAAAGCAGTGAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGTGTGAACAGTGCAGACTCATACACGTGCGAGTGTGCTTGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGGCGAAGGAAGGATGTCTGCAATCAACCCACATGGCTGCCAACACATTGTGTTA
ATAATGGGAATTCCATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGGACGGGAAGACGGTCAAGAAT
GCACGTGAAAGCCAATTGACCTGGCTTTGTGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGAAATTATAGATTCTTGCAAAAGCCCTGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCAAAGACATGAAAAAAGCCGTGGCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGGACGGACGGGCTCAGGATG
ACGTCCTGGAGTGGGCCAGTAAAGCCAAGGCAATGGTACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCTCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAACAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAACGGTCCAACAGCCAACAGAACATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAACAAATCTTACGGCTACACAAAGCTTT
CCCATTCAACAAACCTCAGGAAGGCCCTTGAAGAAAACAGCATCAATGCAAATGAAAACCTTATAATGT
TCCAGAACCTTGCAACAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAACGGCC
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCAGACACATTGTAGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGAACAGAACAGTATAACTACTAATTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAACAGAACAGTATAACTGCAAGGTATTGTAATATACTGTGGACAC
AACTTGCTCTGCCCTACCTCGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTGGATTTTATACAATATTAAAATTCCACACTTCAG

0 1 2 3 4 5 6 7 8 9

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KRMRLSTGTMGLAIQYALNIAFSEAEARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCALKDSCALGDHGCE
HSCVSSEDFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRKDVCKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTRLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCGTACTCCGTCCCGCCAGGGAGGGC
CATGATTCCCTCCCCGGGCCCCCTGGTGACCAACTTGCTGCCGTTTGTTCCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTGCACGGGAGGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCCCTCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGGAGCTGTTGGGTACCCCTGGTGGACTGGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC
TTATTAACATGAAATATGTGTTTTCTATTGCAAATTAAAGATACTAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSRSKP
AVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQC
CNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDI
KEDAIAPRTLWPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSRMGAVPVMVPA
QSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262, 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACGCCAATGAAACGCCTCCGCTCTAGGGTTTCCACTTG
TTGAATTGTCCTATACTCAAATTGACCCAAGACACCTGTCTCCAAATGAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTAAGGATATCCCAGAGCTTCC
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATGGCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATA
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATA
AGAGTATTGGCTTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCATATGCATTTT
ACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTCATGTTGGTGTCACTACAACAAAGGGATTTGCA
CAAGAATTTTATATCTTGGCTATCTAACGCCAGCCGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTCAACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCGGCACCACGGATCTT
GGGGTCTCCATGTTGTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCAGGGATGTTCATTTTATTCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTAAAAATGCCCCGTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAAC TGCAACAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAGTATTAAATCAGTTTCT
GTTATGCTATAGGAAC TGAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCAC TGGGCTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAATTGTTGACATAAAATAAGAATTGAAGAAACACATTTCACCATTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNTLTFEVKTVNNFVQRDTFVVWDKLSVNHRRTHTLMHTVEQATLRISQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTTNKLFCSIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGAATGTTGCAGTGCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCAGTGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGAGGAGTTCCCCGAAACCCGGCG
CTAAGCGAGGCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGTCACCCCGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCGGGGGGAGGGGGCTGGGCTGGGCCGGAGGC
GGTGTGAGTGGGTGTGCGGGGGCGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCCGTGGGCCCCTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGCTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGGTCCACGTATGG
ATCCTGGCCGGCCTGGCTGGCGGGCGCCCCCTGCCCTCTCGACGCCGGCC
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTCCTGCGCATCCGTGCCGACGGCGTGGACTGCGCCGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTCGGGACCGTGGCATCAAGGG
CGTGCACAGCGTGGGTACCTCTGCATGGGCGCCACGCGAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCAGGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCAAACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTCCTGCCATGCTGCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCACCGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAAC
GAGACCATGCCGGCCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCAGTCTGCTTGAATACCTCCATCGATGGGAAC
TCACCTCTTGGAAAAATTCTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACGTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTTGAGAATAACTTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGGCCACGCCCTTGCCACCTCACATGCCCTCCATGGATTGGGGCCT
CCCAGGCCCCCACCTATGTCAACCTGCACTTCTGTTCAAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAAATTATATTATGTATGTAAGTGAGGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHLRPLVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

099605348-024204

FIGURE 23

CCCAGAAGTCAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTTTCCAGATTAGAGTGGAGAAACTGGGTGGAGTGTCCTCTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCG
GATCAAAATGTGACAAGAAGTGATGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTTAATACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATTTC
TGTTGGATATCGCAGGTGTCCGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAATGTGCAGTGGCTCACGCCGTTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATAAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TWTLEVVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
LLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

T03T20**B4E501660

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTTCTCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTATCA
TTTGACAAATGCAAGCATTCCCTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCTGAAAATGTCGACTGAGCAACTACAAGAACTCTATATTAACTACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACATGAACTTTAACGCTCTTATCA
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAGTGTAAATCTCAAATTGGATCTAAATTAAACCTATTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCAAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGTACTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTACTGTGATCCGTG
GATGAACATGAACAAACCAACATTGGATTATGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG
CTCCCTTCTTATAGCTCTGAGAGCTTCTCTAACTCTAAATGTAAGCTGGAGCTATGT
TTCCTTCAGTGTAGAGCTACTGCAGAACACCACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCCTAATACCCGTACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAATGGCGTAACTCCCCAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTGAAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCAATTCACTGGATGGCTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTCGCAAAGTGTGAAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCGTATCAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAAACTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTLGLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQVVNLKFLDLNKPINRIRRGDFSNMLHLKELGINNMPPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLMSNALSAHYHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVT KGLHPDQKE
YEKNNTT LMA CLGG LLGIIGV ICLIS CLSPE MNCDGGHSYVRNYLQKPTF ALGELY PPLIN
LWEAGKEKSTSLKV KATV IGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTTAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACACATTGAA
ACTTGTATTCAGTTTTGAATTATGCCACTGCTGAACTTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMC~~LLQSFVLMILCFHSASMC~~PKGCLSSGGLNVTCSNANLKEIPRDL
PPETVLLYLD~~S~~NQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF~~L~~
NAANDADLCNL~~P~~KKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

T00720-84150660

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGAGATTGCAGGTGAGCAAGAGGAATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT
GGGCTCAGTGCTGTCAGGCTGGCCACGGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTCACCGCAAGTGCTTGTGGCAGTCCCAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTAACCGAGCAGGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGCC
CATCGTCTGGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCACTGGCCACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCATCAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGCAGCTGGCGTGGTGGAGGCCATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGGCCACGCCAGGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTACACTGCCGCC
CCCGCATCCGGGACCGAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTCAGTT
GTGTGCCGGGCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCGTATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGGCCCCATCAGCCAACAA
GACCTTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCCATGGCTTCTCTTTC
CTGGCGTCCTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGGCCCCCAAGTCAACATGAAGATGATATGAGGCCGGGGGGGGCAGGGACCCCCG
GGCGGCCGGGAGGGGAAGGGCCTGGTGCACCTGCTCACTCTCCAGTCTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCC
CCAGCCCTCACCACCTGCCCTCTACCAAGGACCTCAGAAGGCCAGACCTGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACGGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIIILVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNNLETLLIDSNPLA
CDCRLLWVFRRRWRLLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIADRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGGAGCATCGTGTGCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGAACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATAGAGGCGCTGCCACTCCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCTGCATGGCAATTC
CCTCACTCGACTTTCCATAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTAGGATTCTAGTCTCCGGGCCCTG
CCCAAGAAGAGACCTTGCTCCCTGGACCCCTGCCAACCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGAGCTGCGACACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAAATAACATCGTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCCGGGCTGCAAAACCTAGAGTACCTGAACAGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGCA
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCTCCGGACTGCTGCTGGT
GTTGTCACCTCCGCCTTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACCTCCCGCGTCCGAGATTAACTCCCTACAGACAGTCTGT
GAECTTCTACTGGCACAATGGCCTTACAACGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT
GACCCCTTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLSKLEVILNDNLISTLPANVFQYVPITHLDLRG
NRLKTL PYEEVLEQI PGIAE ILL EDNP WDCT CDLLS LKEWL ENIP KNALI GRVV CEAPTRLQ
GKD LN ETTE QDLCPLKNR VDSSL PAPP AQEET FAPGPLPTPKTNGQEDHATPGSAPNGGT
I PG NWQIKIRPTAAIATGSSRNKPLANS LPCPGCSDH IPG SGLKMNCNNRNVSSLADLK
KLSNVQELFL RDNKIHSIRKSHFDYKNLILL DLGNNNIATVENNTFKNLLDRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHN NYFM YLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFM LLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLL VFV TS AFTVVGMLV FILRNRKR SKR RDAN SSASE INSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTCTGTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGTCCGTGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTCGTCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCTCGCCCTGTGCGCTCTGGCAGGCGCTCTGGCCCGGGCGG
CGGCAACACCCCCACTGCGGACCGTGCTGGCTGCGCTCGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGAGGAGGCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCGCTGTGCTCGCCTCTGCGGGCAGGCCAGG
GCCGGAGGGGCTCAAAGACCTGCTGTTCTGGTCGACTGGAGCGCAGGCCACT
GCACCCCTGGAGAACGAGCCTTGCGGGTTCTCTGGCTGTCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGTGCGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTGCGCCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCGCTAGACGACTTGGGAGG
CTTGCCTGCGAATGTGCTACGGCTTCAGCTGGGAAGGACGGCCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGTGCCACCAGGCGCCGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCACCCCTCAAATGTCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGTGGCGAGTCCCTTGGCTCTAGTGATGCA**TAGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACCGGGTAGTGTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPAGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPPEAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATTCA
GCAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCAT
AATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTAC
CCCCGGCTACCTGGGCCGCCCGCGGGTGC
CGCGCGTGTGAGCCAGCGCTGCTGCCAGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGAGCCAGCGCTGCTGCCAGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTTCCCAGAGGAAAAGTAGTCGTTCTCAATTCCGATTCA
TAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCTTGACAGACCTCCGGCTCTTAAAAC
CCCCAACTGCCAGACCGGGATTACCC
CTGCAGGAGTC
ACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAA
GTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGA
TAGTCCACCTGCGCCAATTGTGTCTGAGAGAA
ATGAAC
TTCTTATTCA
GACTTAAGTTA
ACTGCAGATGGGTTATTGGTCA
ACTACATATTCA
GAGGCCAAA
AAACTGCCTACAACTACAGAACAGCCTGT
CACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTTGTGTA
ACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGA
CTTGTATTAGCCGGCACTGTTATCACA
ACCACATCACTCGCAGTGGAGTTG
CACGCCACAGTCTCGATCATCA
ACATCTACAAAGAGGGAAATTGGCGATT
CAGCAGGCAGG
CAAGAACATGAGTGC
CAGGCTGACTGTC
CTGCAAGCAGTGC
CCTCTC
CAGAACAGGTC
TAAATTACATTATTATGGGCAAGTAGGTGA
AGATGGCGAGGCAA
ATCATGCCAACAGC
TTTATCATGATGTTCAAGACCA
AGAACATCAGAAC
GCTCCTGGATGCC
TTAAAAATAAGCAATG
TTAACAGTGA
ACTGTCCATTAA
AGCTGTATT
CTGCCATT
GCC
TTGAAAGATCTATGTT
TCTCAGTAGAAAAAA
AATCTTATA
AAATTACATATT
CTGAAAGAGGATT
CCGAAAGATGG
GACTGGTTGACT
CTTCACATGATGGAGGT
ATGAGGCTCC
GAGATAGCT
GAGGGAAGTT
TGCCTGCTGT
CAGAGGAGCAG
CTATCTGATT
GGAAACCT
GCC
ACTTAGT
GC
GGT
GATAGGA
AGCTAAAAGTGT
CAAGCGTT
GACAGCT
GGAAAGCGTT
ATT
TATACATCT
GTAAAAGGAT
ATTTAGAATT
GAGTTGT
GAAGATGT
CAAAAAAAG
ATTTAGAAGT
GCAAT
ATTTAGT
GTTATTGTT
CACCTCA
AGC
CTT
GCC
CTGAGGT
GTACA
ATCTG
CTT
GC
GTT
CTA
AATCA
ATGCTT
AATA
AAAGG
AAAAAAA
AAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

PROTEIN ID: 34591660

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCCCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATAAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGA
ATCGGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCCPTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKCCPAGTFGPSCLPAGTERPCGGYGCCEGEGRGGSGHCDCQAG
YGGECACQCGLGYFEAERNASHLVCACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCGCCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGCCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAAGGAGGCTCCAGCCATAGGCCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTATTACTGCACTATATTCTAACGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCACCACCACTCTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

POET20-B4E060

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGTATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCCTCTGATAACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCACTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCTGGAAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEEKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGTTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCAACTGCCACCCACCGTCACTCACGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGAACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLLLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCCSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDGPDSDELGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCAGAATGGCTTCAGGACCCCCAGCG
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCGGGTACATGCCCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTGGTTTAGACAAATGTAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

1000 200 300 400 500 600 700 800

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLGATKRLCLKHFNGLGWI PSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGTCCGCTCCGCCCTCCCCCGCCTCCCGTGCAGTCGGTCCGTGGCTAGAGA
TGCTGCTGCCGGTTGCAGTTGTCGCACGCCTCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCTGGCGTGCTGCTGGTGGGCTGCCGCCGACGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
ACAATTAGGAACTGGTATGTGGATGAGCCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCATTGCAAATATTCTGATGAGAAACCAGCAGTTCCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTCTGTGGTCACCACAGTTGTATGTTGGTTT
GGATCTGTAGAAAAGAAAACGGGAGGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGTACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGAAAATACACAGAACAGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTTCCCTGCTCTACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSRAEAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLLLV
VTTVVCWVWICRKRKREQPDNSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTCGCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATACTGGTGT
GTTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCTTTC
TTTCACCAACCTTCACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTTGTATCCAACCTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

1000 900 800 700 600 500 400 300 200 100

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LD MFILNAMS VY TLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

TOEET 20° 24°C 0.660

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC~~GT~~GATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGT~~CCT~~CATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGT~~CAGG~~CTGGCTGACGGCCCTGGCATTGCAAGGGAC~~GC~~GTGGAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACC~~AT~~GATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACA~~ACT~~GGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTC~~TT~~GCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC~~C~~AGCACAGATTTGGGGTT~~C~~ACGACTGCACCCACCAGGAAGA
TGTGGCTGT~~C~~ATCTGCTCAGTGTAGGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAC~~A~~CTGGT~~CC~~CTGATTCTCAGGCC~~T~~CAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA~~ACT~~ACATCA
CCACCTTCCTATGTC~~C~~CACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGT~~T~~
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCA~~TT~~GT~~C~~CTGTTCTGAAGAA~~CT~~GTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAAC~~GG~~A~~TT~~TAAGGATAA~~AT~~TTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATAAAATTCTGGTAAC~~TT~~ATTTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWECEDPDFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIVL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGCGTCCCGGGACCGCGTGGCGGACCGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGCCCTAGAACAGACTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGCAGCAGCAGCAGCAGCAGCAG
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACAGCAGCAGCAGCAG
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

TOEFL TOEFL TOEFL TOEFL TOEFL

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFCGYVDIL
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTGACATCCTC
CTGCTTCTCCCCTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTAACAAATACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAACGATTTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTTGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATATTATTGATTGCACTTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCAATGGTAGGTT
TGAAGGACTATATCTAGTGGTATTCAACATGAATATCATGAACTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSI
YTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHV
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS
GILTEQKMI FIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

TOGETHER 60

FIGURE 59

CCACCGCGTCCGGACCGTGGGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCTGAGAGATGGTGGTGCCTATGTGAAAGGTGATTG
TTTCGCTGGCCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATA
GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTTCACCCCTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGGCTTATGTTGTACACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACTGCACTAATTCAAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAACAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAAGTGCATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTTCGACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACCCATGGTTAAGTGAATAATTATAAGGTTCTGA
TCTACAATGCCAACCTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTCACCTATGACCAGCCTCTGAGAGCTTGCACATGATTAATCGA
TTCATTATGGAAAAGGATGGATCCCTATGTTGGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTTACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA
AATTAGGGTCTTGAATAGGAAGTTAATTCTCTAAGAGTAAGTGAAGGTGAGCTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
VGPFPGNMKSYAGFLTVDKTYNSNLFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFQAFEILDKLLDGDLTSDPSYFQNV
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTTCACTCTGAGAAATCGTGAUTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAAACGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTCCGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGCCAACGCTGGGACTCACTGGCCC
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCCTATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGCCAGTGCACGAAGGCCCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKL IIIDYS ENRLLACGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMGVIVRSEGEGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL A QAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTS VASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GGACTGGAGTGGGAACCGGGTCCCCCGCCTTAGAGAACACCGCGATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCCGCACCGCTGGGACTCCTGCTGCTGGTCCTGGGCTTCCCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTCGGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCGTGTGCCAACGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTTGAACACCCTCACCACTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCCCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCTGCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGAACACTTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCAGGGTGGTGCACCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAAGTGGAGAATGAATATG
GTTCCCTATAATAAAGACCCCGCATACTGCCCCACGTCAAGAAGGCACTGGAGGCCGATTGTGGAACTGC
TCCTGACTTCAGACAACAAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGACTCTGGCCACCATCAACTTGCAGT
CAACACAGGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCCAGGGACTCAGCCCAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTGGATTCTTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACATTGGCTTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCAAGCTATGACTATGATGCTGTGACAGAACGCCGGC
ATTACACGGCCAAGTACATGAAGCTCGAGACTCTTGGCTCCATCTCAGGCATCCCTCCCTCCCCCACCTG
ACCTTCTCCCAAGATGCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCCTGTGGGAGGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCCCTCACACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGATGTCAGGGGAGG
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGGAGAATCGTGGCGAGTCACATGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCATCTGAATGATTCAACCCCTGAAAAACTTCAGAACATCTATAGCCTGGATATGAAGAAC
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGCCAGAACCTTGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGTCATGTTTGAGGAGACGATGGCGGGCCCTGCATTACAGTCAGGAAACCCCC
ACCTGGCAGGAACCAAGTACATTAAGTGAGCGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCCTC
CTCTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCAGCTCAAACCCCTAACGCTGCAGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGGCTTCTACAGCCCTGCTCTGTGCGAGGCTGTCGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCCTTGCCCTCAGAAAAGTGCTGAAACAGTGCCTTGACCGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGAGGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT
CTTCCCTCACAAACCTCTGAGCCTTCTTGGAATTCTGAAAGGAACCTGGCGTGAAGAACATGTGACTTCC
TCCCTCCCACTGCTGCTCCACAGGTGACAGGCTGGAGAACAGAAATCCTCACCTGCGTCTCC
CAAGTTAGCAGGTGTCTGGTGTCACTGAGGAGACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCA
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCAACAGCAGGGGAGGAGCAGGCC
GAAGTGTGTCCAAGTCCGATTTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGGCTACTGCTG
GTTGAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSNDKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPCKMVMEYWTGFDSWGGPHNILDSSVELKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNNGNGQSFYIILYE
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQQGYTVLRIILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

TOP SECRET//NOFORN

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCAGGAC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCCAGGCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCCCTCGTCCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGGTATGACCGGTTCTCTTAGACGGGGCCC
CGTTCGCTATGTGTCGGCAGCCTGCACTACTTCCGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCAACGCCATACAGTTTATGTGCCCTGGAAC
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTGCTCGAAAACCTGAAATTCAAGAACCTC
AGATCCAGACTTCCTGCCAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GAECTATACCACTGTAGATTTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTCCCTCCGATTACTACCACTGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGTCTTCAGATGTCATCAGCAAGT
TCCAGGAAGTCCCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTGCTTGGCCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAGCAGGACCATGGCTCATGTTGAC
GAACCTATATGACCCATACCATTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCATGTGATGGTGGATGGGGTGTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAACGTTCAAGGGCTGTAAGGCCACCAATTCTG
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACATTGGGCCGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCCCTGCTGTTCCCTAGGGAGCCCTAACAAAATT
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCAAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACTTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCTCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCAACTGCACCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSRSVSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGNSSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQOGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

TOP SECRET//NOFORN

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

9
8
7
6
5
4
3
2
1

GCTTGAAACACGTCAGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATT
GCGTCCCTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAATAAACCTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCTAAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACACTGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAACAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATACCCCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATATGACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATTTTAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTTAAGTCATTCAACATTCAAGTAAATTGTTTTCTTTGGGG
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNKMIGLESRLRELRLKILHVKSNLTKVPSN
ITDVAPHLT KLV IHNDGT KLL VLNS LKKMMNVAELELQNCELERI P HAI F SLS NLQ ELD LKS
NNIRTIEEI ISF QHL KRL T CL K LWH N KIV T I PPS ITH VKN L E SLY F SNN K L E SLP V A V F S L Q
KLRCL DVSY NNISM IPI E I GLL QNL QHL HIT G NK V D I LP Q L F K C I K L R T L N L G Q N C I T S L P
EKVGQLSQLTQLELKGNCLDR LPAQLGQCRMLKKSGL VVEDHLFD TL PLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGCCGCTTCTCTGGACTTGATTCATTCCATTGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACATAAGGAT
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGGCATTGCTTAGTGGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCACAGTATTATGCCTGTC
ATCGCTGGTGGTACCTGGCGCTGCTCCTGCTGATAGTTGTCGTCTGCTCTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTCGCTGTAaaaATCACAAACCGACAAAGGTGTGGTGGGCAAG
AACAGCCAGGCCAAAACATTGCCACGGAGCTTGTGCGACATAAATGAGGGCCTGAGTTAGGAAAGGCTCTCTCAA
AGTTTGATTCCCTGCCACCTTGCTGCGACATAAATGAGGGCCTGAGTTAGGAAAGGCTCTCTCAA
GCAGAGCCCTGAAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCCTGCTGGGACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTGGGAATGCTGATAAAACCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGCGAGCTGACAATGGGGAGGCTGAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCAATATGGCAGAGACCCACAAGGCCATGATCCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAAGCTTTGACGGAACCTCCAGCAATGGGCCTGCTAGGG
CAAGTCTGCAGTAAAAGACTATGTCCTGATTTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCCTTGCTTCTACTACTTCTCTCCTAACATCTTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAAGGATCCTTCAACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACATTGATTCTTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTCACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTAACTCTAATGGGAAATAACTTGCAC
GACCCAACTTGCAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTTAAATGGATGTGGTACAATCAGA
AAGGTTAGAAGATCAGTCATTACTTACACCAATAATCACCTTCTGATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATCAAAGTCAAATGCACTGGGAAATATAACACAGCATGGCTTTGAATCCAATTCA
TTTGGAAAAGACTATACTTGAATCACCATATTATGTTGGAACCAACTCTTGTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATCACCTGTAGAGCCTCTCCACCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGGTACCTGCTCGCTGCAATCAAGGGTGTGCTCCAGAAGCAACAGGAGACATTCTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAAGTGGCAATTCAAGGATTCAGCAG
GAAACACATGCCAAGAAACTCCAAACCGCCCTTCAACAGTGTGATCTGTTCTCATGGTTCTAGCTCG
AATGTGGTACGTGAGCGACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCATGTAAAAAAA

FIGURE 70

MELVRRLMPLTLLIISCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDPGSCESENIVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDG PSTNSGLIGQVCRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVRSRKDISSYWKTDIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCAAGGAGCTCCCAGGCTCGCGTCTCGCTGCTGTTGCTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCAGGGACTCGGCATCTCATCCACTG
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTCCCCAGCTCGTAGCGAGTGGTCTGGGGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGAAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTCCAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTGTGGGGT
CAGAATATTGTGGAACCTGGATGCCATAGATGAGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCATTAGGAACAGAACTGACCTGCCTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTTCAG
TTTCTAACAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA
CATAAATGGAAAACATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAGCTGG
AATCTCTGACTATCTACAAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATGGCAGTTCCAGTGCACTTGCCATTAAAGTC
AATTCTTCTAAATTACCCATGTAACCATTTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG
CTTACAGGACTGGAAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAAATTAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPWESLDARQLPAWFDQAKFGIFIHG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNTQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATA
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCTTTGCCTGCAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACCGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCTATTGTTACAACATCTGAT
ACTTGGACTAATCGTCATTCCAGAAATTATCACCAACAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACAGTACACTCGGTGGCATCCCC
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGGAAACTAGCACCATTGTCTACAGAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAAGCAAAACTACCGTGCATGCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAGAACAGAAAGTCCACCC
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAC
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC
TTCTAGCCTGGCTATGTCCTAATAATATCCACTGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA
AGAGCAAAAGAACGGAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAATTGCACATAGTAGAACGCTATCTGGAAAGCTATTTTCA
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTTATTGCTGAGACTAATCTT
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAGAAC
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISP NPKCGKNGVGVLIW KVPVRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

1000 900 800 700 600 500 400 300 200 100

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGAACATATAGGAAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGC
TTGGTCTAATGACTGCCATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACA
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGG
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCAAGTGT
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCCTGT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGCTGGTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCACTGGAGCAAGAAAGAGATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCAGGACTCTGCTTCAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDI RMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFKGKV DVG RYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAV SWTFSE
ENVIREFNLNEL YQRAKKLSKAGDNI PEEQP VASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCCCAGAGAACGGACGTGCTGGTGGCCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACCAAGTCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTCTCCGGGCTGGAGGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCTGGAAGTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTTCACCGCATCCTAACTGTGGCCCCAGAGCCTGGGT
CCGAAGCTTGGCTTCCCCGACCCGAGAGCCGCTGTACGGTGTAACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTCTCAATTAAATTCT
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGTGGCTTCTG
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC
CAGCCTGGGGAAAGAACGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGATCTGAGGGAAAGAACCTCCCTCCCCGTTCCC
TCCCTCTCGGTTCAAAGAATCTGTTGTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

MGLLLVPLLLPGSYGLPFYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGACCGGATGATGTGGCACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGACACGTACGACACGGACCGACGGCGTGTGG
CATACGGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGACGGCGTGTGG
GTTGGAGGAGCTCGCAACGCCACCTATGCCACTACGCGCCGGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGACGAGCGGCGTTCCGGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCGCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT
GGCCCCAGCCCTCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTGCGCTCCCAG
CCTGTCGTCGTCGTTGGCGCCCCGCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCCGAGGGCGCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCGTCGTTCTCTCCCTGTGCCGCCGCCGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCCGGGCTCCCGCACCCCTGGCCTGCCCCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGGCCCGGGCAGCGAGGGAGGCCCTCCATTGCTATCACATG
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCCTGCCCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTGATGGAACATAGTATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTACAGTAACAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG
CAATAAAGATTGTAAGCAGACATTGCATTTGATTGATGAAAGCTTAATATTGGCAGC
GCCGATTTAATTTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTTCAGTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCCAAAGTGGTGGTGGTATTTATTGATGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTGCGACTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAATCTGAAATGCTTACTGATAGAATCAGATAACAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCCKADIAFLIDGSFNIQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIACLI
DGSSSVGDSNFRLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPIPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCCGGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTC
GGGCGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGACACGCAGCACAAATTGCGCAGCGGGTGAAGAGATGGAGG
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGGGTGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCAGCTGTGTCTGGGTCAGTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTATGGAGGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCT
GCACGTGCTGGAGGGGAAGAGATT**TAGAT**CTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAAGGCTTCCCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGCAATTGTTAGC
TCCCCCAGGCTGTTCCAGGCTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCGATTACATGTGTTATTGATCC
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCCTCGCCATCAGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCCACTACCCACACCGCCTGGTGCCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAAATCACTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACACTCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTGATAGAAAAGGACAC
TAAAGCCTTAAGGCAGGGCTGGCATTACCTCTGCAGCTCTGGCTTGAGTCAAAAAACATGGGAGGG
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTGGAGAACCCCCATCTACTAAAAAATACAAAAATTAGCCAGGAGTGTTGGC
AGGTGCTGTAATCCCAGCTCAGGTGGCTGAGCAGGAGAACATCGCTGAAATCCAGGAGGGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCTAACACTCTGATCCTCTTCCAGGGCTGGCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAACGGCATATTGAGGAGGGCAAGAAAGTGACGCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCCCTGGGAGGGTGTGACCCCTACCCCTGCAAAACAC
AAGAGCAGGACTCCAGACTCTCTGTGAATGGTCCCTGCACTGAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGTCTAGCTGGGGCTGGTGCCTGCACTGCACTGTGCCCTGGTACCCCTGGCATGTTCCCTGCCCCCTCA
GTGTGCTGCCAGATCGGCCCTGGTATACGCCCGCTGTCCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGTCAGAGCAACAGCATTGT
CCGTGTGGACCAGACTGAGCTGGGTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTGG
TGCCCGAGACTGTGATTTCCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACCGAGCTGACCGGCT
GGAGGACACAGCTTGCAAGGGCTGGCAGGCTACAGGAACCTATCTCAACCACAACCAGCTCTACCGCATCGC
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGCCGTCACCTCAACTCCAACCTCTGAGGGCCATTGACAG
CCGCTGGTTGAAATGCTGCCAACTGGAGATACTCATGATTGGGGCAACAAGGTAGATGCCATCCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCTATGACAACCAGCTGCCCGGGTGCCCAGGCGGGCACT
GGAACAGGTGCCGGCTCAAGTCTTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC
CAACATGTCACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGCTCCATGACAAGTTGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGCGTGTCCCTCATCACCCCCCGGCCTTCA
CCACCTGCCCAACCTGCAAGGAGCTCCACGCAACACAGCTCTCAGTGCCTTGCAACAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGAGTAGGTCTCCACGCCAACCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGC
CACGGGCACCCGTGCCCTCATCGAGCCGAATCCACCCCTGTGCGGGAGGCTCCGGACCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
CCTCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAGGAGGTTACGGGTGACCCCGAGGGACCC
GGAGCTGGAGGGTAGCAGCAGAACAGGAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGGCGGTGCTCTCTCCAGCCAGGAGGGAGGAAGGACAGGGGCTGGAGCTCCG
GGTGCAGGAGAACCCACCCCTATCACATCCTGCTATCTGGGTACCCCCACCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCCTGGGGAACCCACAGCTA
CAACATTACCCGCCTCTCAGGCCACGGAGTACTGGGCTGCCGCAAGTGGCTTGTGATGCCACACCCA
GTTGGCTTGTATGGGCCAGGACCAAAAGAGGCCACTCTTGCACAGAGCCTAGGGGATGTCCTGGGCTCAT
TGCCATCCTGGCTCGCTGCTCTCTGGCAGCTGGCTAGGGCCACCTTGGCACAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGCGCCTCTCCAGCCTGGCTTCTGGGCTGGAGTGCCTCTGTCCGGTTGT
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAAATTCTTGAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACAAA
AGAGAACAGTCTGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTGAGGCCTGGCAGCTGGC
CAAGACAGATGGGCTTGTGGCCCTGGGGTGCTTCTGCAGCCTGAAAAAGTTGCCCTACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCATCTT
CTCTCTGCCAGAGGCTCTGGGCTGGCTTGTGCTCTGCTCTGCTCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTCACCTCCCCAACCCGATTCACTCTTCTCTGTAAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSIVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGALKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGVADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGGRRLPWAFAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGGCTGTTGAGAAGGTGAAGAAGTCCGGACCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGCTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGCCACACTCTTCAAGATCCTGGCTCCTCTACATCAGCTAGTCATCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTTCTGCGAGGTGAGTGGAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCTACCAAGAACCGCGCAGGACAAGCTGGAGCTGCACCTGTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCGCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTTACCAACAGCGCCAAGATTGAAGCGCCTGCC
GGCCTTCTGCCGAGAACCTGCGGGCGTGCACATCAAGTTCACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCTGAAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGGGCGGAGAACAAACCGCTACATCGTCATCGA
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGTGCTGCCGCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTAC
AGATGTGGCGTGCACCTGACAGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATTTCA
GAAGATGGCGAACCTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
CCACAACTGCAAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCTCACCTGCCCTAACGCTGCTTACAGCTGTGGTACAACCACATGCCCTACATCCCCATCCAGATCGGCAACCTC
CCTGGAGGCCCTTACCTGAAACCGCAACAAGATCGAGAACAGATCCCCACCCAGCTTCTACTGCCAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTGCCGACATCGGCCCTGCGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGCCAGACGCTGCCAG
GGCAACAAACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGGAGCTGACCAACCTGACGCAAGATCGAGCTGCC
CAACCGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCTCAGGCCGGAGGGGAGGCCCTAGCTTCTCC
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGAGCCTGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGCCCTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCTAGGGCTGAG
CTGCCACCAGAGGTCTGGACCCCTCACTTAGTTCTGGTATTATTCTCCATCTCCACCTCCCTTCTCATCC
AGATAACTTATACTTCCAAGAAAGTTCAGGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTTCCCC
TTGTCTTATTAGCGATGCCGCCGGATTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGCGAACCCAG
CCATGGGAGGGTCAACCGCAGTGCCTGGCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
AAGGCCAGGCCCTGGAGCTTGCCTCTCAAGTTGTGGCAGTTAGTTAGTTTTGTGTTTTTTTTTTAAATCAA
AAACAATTTTTAAAAAAAGTTGAAAATGGATGGTTGGGTTAGTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG
AAAAGACACTAACGCCAGTGAAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACAGT
TGAACGTGTTCTTCCCTGGGCCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT
CTATTGTTCTGGGGAGGGAGGTTTTGTGTTGGGTTTTGGGTTGGTGTCTGGTGTGTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTCTGTGGCTGCGCCAGGGAGGAGGAGGAGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCCATTGCCACCTCCCTCGTGCCTGCCCTGCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCCAAGACTTGTGTTCCCCACCTCCCTGCCAGGGTGT
CCAGTGCCACCGCTGCCCTCCGCTGTTCCATCACGCCCTGCGCACCTGGCTTCTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGGAGGCTGCCCTGGAGGGCAGGCCTGGTGGTCCAAGGCCGGTCCCTGGCG
CTGGAGTGCACACAGCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTTAGATCACTGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTGTGTTCTCGCTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACATTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYVHNIFDVEDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVLDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAAACCTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCGTGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTGCAGGGGGT
TGCCTGGGTGATT CCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT
ACAGCATGTCCTCTCGAACGACAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTAGGAGGCCTG
GGTGGGAAACTGAAGTGGCCAGAACCTGCCTAAATTCAAGTCAGCTGAAGTGGAGGCCCTGT
ACAGTGACCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAUCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAACGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAACCTAACGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLP~~LLL~~GLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKG~~L~~AEVSKVAEQVLNAVNGLYRE
ATELGKAEMIIEQNTDGVN~~F~~YNILTKSTPTSTM~~E~~SSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGTATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGAAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGAGTAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDSLDPGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGGCCGACCAGCGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGGCGACCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAGACTCTCGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGGGCCATCCC
CACTGACCCCTCACACGGTGCAAAATGGCTTGGCAGCCGGAGGCCAGAAGTGCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACTACGGAAACCCATGTTGAAGGTCCCCAC
ATCCCTACCAAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTTCCGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCTGCTTCCGCTCAGGTGACAGT
GGGGCCGGGTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCCAG
CCCCTATGTACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCCTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGTGAAGACTCTACTCAACCCCTGACCCTTCCAT
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCAAAGGGTTGTATACAGACTCTGTGCACCA
TTTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAAGATTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

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GCCGCGCGCTCTCTCCGGGCCAACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGGAAC
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGAAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGCCAGAACATTCACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAAAGTAACTTCACGTTTG
CAAACTTGATTTCATCTGAACATTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIDHGKTYVKG
TQKLRVGFLKPDKDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKGWI
KGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFGSYDNDRPGNLVYRFCDV
KDETYDLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCAACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCTGCAGAACAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT
CTGTACTGGGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAACGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGGCGCTCCTAGGGCGCAGCGGGACGCCGGCTCGGATCTGAAAGGGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCTCGGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTATTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCCTCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLF SVLLGA WQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPI IDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGI ISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCCCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGGCCCAGGTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAACTGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCCTAGCAACGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCTGG
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCAGCTGTCCTCCTGTCATCTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAAGGAAAGGCTACGGGCATGTGCCTCATCACACC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGGTGGGGAGGCAGGGACGAGGAAGTAACTCCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLTVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAGTCAGGCTTTCATTGGGAAGCCCCCTCAACAGAACCGGCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAAGTGAACAAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTCCCTGAAACTTGGACCTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGCCAAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAAAGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAAGTCTGAAATGCAAAGAACGGAGTAAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCACTGGACCATAACAACTAACAGAGATTACAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTCAACTTCAAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGAACACAGACTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCCGGACTTAAAGACATGAATGGTGCCTTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCTTTGCGATTGCCAGCTAAAGGCTCCACAGTGGGGGGGAAACAAACTT
TCAGAGCTTGAAATGCCAGTTGCTGCCCCATCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCCAGA
TGGCTTGTGTGATGATTTCACAGGCACTGGGAGAGACGATGCTGCTGAGTCCCAATGACTTTGCTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACAC
CATCCTCGGCTGCGGAGGTGGAATTGCACTGAGGGAAATATCAGTGTGTCATCTCCAATCACCTGGTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGATGCTGATGCCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGCTCTAGAAACACCATCATTTCAGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGGT
AACCGAGAGGACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGCTGGAA
ATACACATGTGAGATGCTTAACACCCCTGGCACTGAGAGAGAACGTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCATGAGTGCACGCCCCATCGTTAGACGATGACGGATGGCCACTGTGGGTGTCGATCATAGC
CGTGGTTGCTGTTGGGACGTCACTCGTGTGGGTGTCATCATACACACAAAGGGAGGAATGAAGA
TTGCAGCATTACCAAACACAGATGAGACCAACTTGCAGAGATATTCTCTAGTATTGTGTCATCTCAGGGAACGTT
AGCTGACAGGAGGAGATGGGTACGTGCTTCAAGAAAGTGGAAAGGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACCAACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGACCCAAAGAACAGTTTAATGGACCACTATGAGCCAGTTA
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCCAGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAAGC
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGAAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACACTACAGGACTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAAATTAAAAGGATAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAATTATGAAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACCTTGTGTTATGCAAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTTATGATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT
TTAAATAGAAGTTACTTCATTATATTGCACTTAAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQOLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLSLEDDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPPQWAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFIVDVKIEDIGVYSCQAQN
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTER
HFFAAGNQLLIIVDSDVSDAGKYCTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLEDDDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD
RQDGYSSESSESGSHHQFVTSAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGTGGCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCCGGGGGTTGGTGTGTTCTGACATAAATAAAATCTTAAAGCAGCTGTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCTTCTC
TATAAAGGAGAAAGTGAAGCCAAGGAGATATTGGAAATGAAAGTTGGGCTTTTAGTAAAGTAAGAAGACT
GGTGTGGTGGTGTCTTCCTTCTTGAATTCCCACAAGAGGAGAGGAAATTAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCAGCAGCACAGTTGGA
TTTGTGCCATGTGACTAAAATTGACGGATAATTGCAAGTGGATTCTCATCAACCTCCTTTTTAAAT
TTTATTCTTGGTATCAAGATCATGCGTTCTCTGTCTTAAACCACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACGGACAAACACCAGATAAAATTATGAAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCATTGACCCCCCTGCTGTGGTCT
GCTGGCTCTTCAACTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGTGCTCTGCCAGCAA
CCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGGAAATTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTGACATCGTCTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGTT
GCGAACAAACCCATTGAAAGCATCCCTCTATGCTTTAACAGAATTCTCTTGCCTGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACTTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGGAAATCA
TTTATCTGCCATCAGGCCCTGGCTCTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGTG
TAACACTCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAACATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTCAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTCACAAATGTAACGTGCAAGATACAGGCATGTACACATGTTGAGTAA
TTCCGTTGGAATACTACTGTCTCAGCCACCTCTGAATGTTACTGCAAGCAACCAACTCTCTTCTTACTTTTCA
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGACGGGACACAGATAACATGTGGGCTCCACTCC
AGTGGTCGACTGGGAGACCAATGTGACCACTCTCACACCAACAGGCACAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGCTGATGAGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCAACTATAACTCATACAAATCTCCCTT
CAACCCACACAAACAGTTAACACAAATAATTCAATACACAGTTGAGTCATGAACCGTTATTGATCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAAACATCAAAAAAA
GACAGTTATTAACATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTTATTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLELDLTFNHLSRLDDSSFLGLSLLNLTIGNNRVSYIADCAFRLGSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRRLLIQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQLHLNTSSLLCDCQLKWLPPQWVAENNQSFVNASCAPQQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA
GSISANATLTVLETPSFLRPLLRTVTKGETAVLQCIAGGSPPPMLNWTKDDSPVLSVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHPSEESCRSFSNISWPS
HVRKLLNTSYSNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCTTCGGCCTGTGGGCGCCGCTCGGCCGGGGCGCAGCAGGAAGGGAGCTGTGGTCTGCC
CTGCTCCACGAGGCAGCCACTGGTGTGAACCAGGGAGAGCCCCTGGTGGTCCCGTCCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGGAAGGCAGGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGAGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGCACCCCTGAGGCACCATGGCCAGAGGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCACAGCTCACCTGGGACCTGTGCTTGCGTGGAGGCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGTGCTGTTACTGAGCCCTGAGG
AGCCCCGGGCTGGCCAGCGCGTCAGCTGCCCGAGACTGTGCTGTTCCAGGAGGGCGTCGTGGACTGTG
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCGCTGAGCACACCAACCACTATCTGAGAACACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGGCTGACCCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCCAGAGAACGGCGTTGAGCATCTGACCAACCTCAATTACCTGTAATTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTCTGACAAACGCCCTGATCAGTGTGGCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAAGACCAAACCTGAGGTCTGTGACCTGACAAACAACAGCTGGCAGACGCCGGGC
TGCCGGACAAACATGTCAGCGCTCCAGCAACGTCAGGCTCATCCTGTCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGACAAAGCTGACACCTCAAGAACAAACAGCTGGAGAAGATCCCCGGGGCCT
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGACAAACAACTACCTGACTGACGAGGCCGTGGACAAACGAGA
CTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTCGGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACTGGAGAAGAACGCCATCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGACAGCAACAGCTGCCAGGCCATCCACCCACTGGCCTCCAGGGC
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACCGCGTGGAGGCCGTGCCAGTGGCCTGCCCTGCGTGC
GCACCCCTCATGATCCTGACAAACAGATCACAGGCATTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGCACCGCGACGCCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCATGGCTGAAATGTCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCATTGGCACAGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCCTGGGCCCCGTGCCCTGGTGGACCTGCCCATCTGAGCTGCTGGAGCA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCAGTGAGTACCTGACAGAACAA
AGATTAGTGCAGGTGCCGCAATGCTTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGACAGTGCCTTCCGGAGGCTGAAGCAGCTGCAGGTCTTGACATTGAAGGCAACT
TAGAGTTGGTGAACATTCCAAGGACCGTGGCGCTTGGGAAGGAAAAGGAGGGAGGAGAACAGGAGGAGGAGG
AGGAAGGAAAACAAGATAGTGACAAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGA
CTTTCTGC
AGCACACGCGCTGTGCTGAGCCCCCACTCTCCGCTGCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGCTCATATCCCCACCCCTCCACGGCGTCCCACGCCAGACACATGC
ACACACATCACACCCCTCAACACCCAGCTCACAGCACACAAACTACCCCTCAAACCAACAGCTCTGTCACAC
CCCCACTACCGCTGCCACCCCTCTGAATCATGCAGGGAGGGCTGCCCTGCCATGGCACACACAGGCCACCA
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACATGCAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGGCCAGCCAGAATGCCATAGCAGCTGCCGTCTGCC
GTCCATCTGTCGCTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCCTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATTCCCTCCATCCTATGGGGACAGGAGCCCTCAGGACTGCTGGCCTGCC
TGGCCACCCCTGCTCCCTCCAGGTGCTGGGAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTCAATGGGCAAGGCCAGTGGAGGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGGCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACACCTT
GTTCTCAGGCCGTGGGGAGTTCCGGGTGCCATTATTTTATTCTTCTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAACATAATAAAAGCATTCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPVLVLSPEEPGP GPAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTN NYLYLANNK
LT LAPRFLPNALISVDFAANYLT KIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSDANVLPIRSLEYLLLHSN
QLREQGIHPLA FQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDL SGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANA FDSTPNLK GIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCCCTGCCGCTGTCTCCGGGAGCGGCAG
CACTAGCCCGGGCGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCCCTCCATGGGCCACCACCC
CAACCTGTTCTCGCGGCCACTCGCGCTGCCAGGACCCGCTGCCAACATGGATTTCCTGGCGCTGGT
GCTGGTATCTCGCTCACCTGCAGGGGCCCGAGTTGCAGGGAGGTGGCCCAAGGCAAATAGTGTCTCGAT
TGGCCTATGTCGTTATGGGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTTGGGGACAGTGTCTAGCC
TGTGTGCCAACACGATGAAACATGGTAATGTATCGGGCAAACAAGTGAAGTGTCTCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGAAGCAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTACTGTCTCACGGATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCACTGGCTGTATGGTTAAAGGACAAATACGGTCCAGTGCCCATCCCTGGCC
GCACCTGGCTCCGTATGGGAGGACCTGTGAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTCTAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGCTGATGTTATAA
CGTACGTGGCTTACAAGTCAAATGTAAGAAGGATACCGGGTGAATGGACTGACTTGTGTATATCCCAA
AGTTATGATTGAAACCTTCAGGTCCAATTGTCAGGAAATGGTACCATTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGTGTTGGAAGTACTTGGTGGCTCCGAAGACACCATATATTCCCTATCATTACCA
CAGGCCTACTCTAAGGCAACAAAGACCTACACCAAAAGGCAACACCAATTCTACTCCACCAACCCAC
CCTGCCAACAGACTCAGAACACCTCTACCAACCTACAACCCAGAAAGGCAACCCAGGACTGACAACACTATAGC
ACCAGCTGCCAGTACACCTCCAGGGAGGATTACAGTGTGACAAACAGGGTACAGACAGACCCCTCAGAAACCCAGG
AGATGTGTTGACTGTTCTGGTACACAGTGTAAATTGACCATGGACTTTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGACGCTGGTGTACCTCTGGCCCTCATGCATTAGGGACCTGTGCTGTATTCAAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGT
GGGAAGAAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACTGGGATTATTGAGCTGGAGAAAG
AGAAGACTGAGGGCAAACCATTGATGGTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAGGAAATTAGA
AAAAAATTGTCATTAAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCCCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAATCTTAGAACTAAATAATTGGACAAGGCTTAATTAGG
CATTCCTCTTGACCTCTAATGGAGAGGGATTGAAAGGGAGAGGCCACCAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGCAATCTAGCAGTATTAAGAAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTGGTACTGCAATGCTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGGTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAAACAGTGTAGAGAG
ATTTCATGGGTGCAATTCTCTGCTGTCAGAACATTCTGGCTGAGAAAAGAGTGCCTGCC
ACACCGGCAGACCTTCTTCACCTCATCAGTATGTTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATTTTTGAAACATAGTACAATAGAAGGTTCTGTGTTCAATTAACTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCTTAAGCCTTGGTAAACGGCAAGAATATGGCTGAGATCCATTAAATGGTTCAATT
TCCTTATGGTCAATAACTGCACTGAGATGAAAGGGAAAATAATGAAATTCTTACTTTGCTGAGAG
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAAATGGCTAAATAAAAACAATTATTGTAATAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASSTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPA GGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGC~~A~~ACAGGTGCTTGCTCGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGT~~CAGGCC~~CTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
CACAATGCCAAATACTTA~~C~~TGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAAGTTCACCATGATGCCACCCAA~~T~~G~~C~~ATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATT~~C~~AGGAA~~T~~GGAA~~T~~CTATCTGCCAGTCA
GAAGATA~~C~~ACAAGTCACGGTTGATGATCCTGT~~C~~ACAAAGCCAGTGGTG~~C~~AGATT~~C~~ATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCC~~T~~GACATGCCATGTGGAA~~GGGG~~CA~~T~~CGG
CTAGCTTACCAATGGCTAAAAAA~~T~~GGGAGACCTGT~~C~~ACACCAGCTCCACCTACTCCTTTC
TCCCCAAAACAATACCC~~T~~CATATTGCTCCAGTAACCAAGGAAGACATTGGAA~~T~~ACAGCT
GCCTGGTGAGGAACCC~~T~~GTCAGTGAATGGAA~~T~~GT~~A~~TATCATTGCCATCATATTAT
GGACCTTATGGACTTCAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGT~~G~~TTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGC~~T~~CGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAACAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAA~~T~~ATCACTATTGATT
ATATCCATGTGTCTTCTCCATGGAAAAAATCAACCC~~T~~ACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGT~~G~~TTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGT~~G~~TATGGGCAAGATTG~~C~~ACAGTACAGT
GTATGAAGTTATT~~C~~AGCACATCC~~T~~GCCAGCAGCAAGACC~~A~~TCCAGAGT**GA**ACTT~~C~~ATGG
GCTAAACAGTACATTGAGTGA~~A~~ATTCTGAAGAAACATT~~T~~AAGGAAAACAGTGGAAAAGT
ATATTAA~~T~~CTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATT~~C~~TTACA
TGCAGAA~~T~~AGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATA~~C~~ACAATGT~~C~~TT
GTGCAACAGAAAAACATGTTGGGAA~~A~~ATT~~C~~CTCAGTGGAGAGTC~~G~~TTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCC~~T~~CATAAGTTGTATGAA~~A~~ATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTG~~T~~TCACCTACAAA
TGTGGAAACTTACATTGTTG~~C~~ATT~~T~~TCAGCAGACTT~~G~~TTTATTAA~~A~~TTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATT~~T~~ATTCCAA~~A~~TTTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGT~~C~~ACAAAAACAA~~A~~ACTATGCC~~T~~CTCTTTTTCAATCACC
AGTAGTATT~~T~~TGAGAAGACTTGTGAACACTTAAGGAA~~A~~GTACTTAAAGT~~C~~TTATT~~T~~TA
TTTTTTCAAGGAAAGATGGATTCAAAATTATTCTGTTTGT~~T~~TTAAAAA~~AAA~~AAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPHPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTCAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCTGCT
TGTAAAACTCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTGAGGTTAA
TATTGCAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGAAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACTGCACAACCTTGAAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTGGGTCCATCATTGCCACAGATAATCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCTTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAGGGTTCTAGTCTAGATTGTCATTAAATTGAAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTTACAGTTGAAATATGATTTAACAGTATGATG
GTTAAATAGTTCTAATTTTGAAAATCGTGCAAGCAATAAGATTGATATTGATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCATTAT
TGAGGTATTAAGAAGATTTTTAGAGAAAATTCTCATTTGATATAATTTTCTCTG
TTCACTGTGAAAAAAAGAAGATTTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTTTCAGTGACAATTCGGTCTTTAGAGGTTATTCCAAAATTCCTTGT
ATTTTTAGGTTATGCAACTAAAAAACACTACCTTACATTAATTACAGTTCTCACAC
TGGTAATACAGGATGCTACTGATTAGGAAGTTTAAGTTCAGGTATTCTCTGATT
CAACAAAGTTGATTCTCTGTATTTTCTACTTACTACTATGGTTACATTTTTTATT
CAAATTGGATGATAATTCTTGGAAACATTTTTATGTTTTAGAAACAGTATTTTTTGTT
GTTCAAACTGAAGTTACTGAGAGATCCCAAATTGAACAACTGTTTGTTAATTAAAATT
TTGGCCACTTTTTCAGATTTCATCATTCTGCTGAACTTCAACTGAAATTGTTTTT
TTCTTTGGATGTGAGGTGAACATTCCGTATTTTGTCTGATGTAAAAGCTTGGT
TTTTACATTTTGAAATTCAAAGCTTAAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTTGTTATGTCTTAAATGTATTTTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTACAGTCTGTTAATGCTGTTGATGTTTAAAATAAACATTTTTATATTTTAAAAGACAA
ACTTCATATTATTCCTGTGTTCTTCTGACTGGTTAATTGGTGGGATTTCCACAGGAAAA
GTCAGTAGGATGGAACATTTTAGTGATTTTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAACATACAATGAATCAACTGACCATTACGTAGAC
AATTCTGTTAATGTCCCTTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTTAATACAAAGTTTCTTAAAGCCCTCTCTTAGAATTAAATATTGACCTT
AAAGAGTTGGATGTGTAACTGTGATGCCTTAGAAAATACCTAAAGCACAAAAAC
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCCAGCTCGGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGCGGAAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTCAGTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGAGTTCTCCCCACTGATGAGGACGGAGATAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGAAATCTGGTACTTGTGAGCAGTTATTGGA
GGAAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACGTACACCCGTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTGCACGAGCCACCGTTGTGATCCAAGACAGGAGTCTCACTGTGCCAGCTA
CCGGGTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCCGAGTAAATC
GTGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGAGCAGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGGTCTCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCCTTCTGTCTCCCTCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCACTGAAACCAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAATGCCCCACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDIYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPOLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPLGAAIWPKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCCTCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGTCTGGAAAGCCAGCGGGCCTGCTCTGTCTTGGCCTCATGACCC
CAGGTCTCTGGTAAAAGCTACTAAGGCCACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAC
ATCCCCTGTGTCAGGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATTGTCCTACTACAGGGACCCACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGGTACTCTACTTCACTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTATGTCAGAGACCCCTGC
GCCACCTTACACACACTTGGGCCACTACGACTGGTCTCATGCAGGATGACACATATGTGCAGGCC
CCCGCCTGGCAGCCCTGCTGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCATG
GCGCAGGCAGGAGCAGGGCCGGTACTGTCACTGGGGCTTGGTACCTGTTGTACCGAGCTCCCTGCTGCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTCCCGTCTGACGAGTGGCTGGACGCTGCCATG
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACCTGGCCAAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCCCTGAGTGCCTTCCGGCTGACCCCTGTCTCCGAAGGGTACCCCTCATG
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCAGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACACACACTCGCTTGAGGTGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTGCAGATGGG
CTCCCAAGTGCCTACTACAGGGGCTAGCAGGGGAGCTGGTGTGAGTGCCTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCCTCCAGAACAGCAGCAGCTCAACGGTATCGGCCCTGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTTGGAAATGTGTGACACAGCGTGGCACCGGGCCCTGGCTCGCA
GGGTAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGGTGTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCGTTGCAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGCCACGAGAACGGTGGCCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAGCAGCGAGTTAGAGCAGGGTACCTGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTCCAGGTGCGACTCATGGACGTGGCTCGAAGAACACCTGTGGACACTCTCT
TCTTCTTACCAACCGTGTGGACAAGCCTGGCCGAAGTCTCAACCGCTGTGCATGAATGCCATCTGGCT
GGCAGGCCCTTCTCAGTCCATTCCAGGAGTTCAATCTGCCCTGTCAACCACAGAGATCACCCCCAGGGCCCC
CGGGGCTGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGCTCCTATAGGGGGAGATTG
ACCGGCAGGCTCTGCGGAGGGCTGCTCTACAACGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTCTCGGTTCTCAGGGCTCC
ACCTCTTCTGGCCGTAGAGCCAGGGCTGGTGCAGAACAGTTCTCCCTGCGAGACTGCAGCCACGGCTAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCGCCTGGGGCCCTAACCTATTACCTTCTGCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

1000 900 800 700 600 500 400 300 200 100

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEFFIGAGEQARYCHGGFGYLLSRSSLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPHQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPLL
VAEAAAAPAFLEAFAAVNLEPREHALLTLLLVYGPREGGRGAPDPFLGVKA AAAAE LERRYPG
TRLAWLAVRAEAPSQVRLMDVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCACTACGTTGCTATGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGATAGGACGTGTTGTCATTATTGTTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAAACTATTAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTGTAAAAAT

FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENKYFLLKKDPSPQFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACGCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCTGTTCATCACCAGATGTGTTGACATTCGCAT
CTTCAACCTGTGATGAGAAAAGTTCACTGAGAATTTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCACTGAGAATTGTTGTCATTGAACGGAAATTTCACAGAGCTCTCCTGCT
AGCTGCTACTTCTTTCTACTGACACCATTCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTTTAAGAACAGAACGGACAACCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCCCTCAGCAACCCTGACATGGCGCTGAGGCAGGCCACCGCGAC
TCCGGCTCTCGCCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTCAAGGGCTGCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGC
AGACAAGTGAACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGTCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCAGTCAGGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGACTTGGTGTCACTGCTG
TTCACAAGGACACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGTCTGACTGGCCCTGA
TCACGTTGGCATCTGCTGTGCATAACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGGCGACTTCAGACACAAGTCATGTTG
TGATCTGAGACCCGCGGTGCTGAGAGCGCACAGAGCGCACGTCACATACTCTGCTAGAAAACCTCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGGCTTTGCTTGGCAAAGTTGACCA
CTACTCTTAACTCTAACAGGCCATGAATAAGAAGATTTCCTCAAGATGGACCCGGTAATATAACCACAA
GGAAGGCAAACCTGGGTGGCTTCACTGAGTTGGGTTCTAATCTGTTCTGGCTGATTCGGCATGAGTTAGG
GTGATCTTAAAGAGTTGCTCAGTAAACGCCGTGCTGGCCCTGTGAAGCCAGCATGTTCACTGGTCTT
CAGCAGCCACGACAGCACATGTGAGATGGCGAGGTGGTGGACAGCACCAGCGCATCCGGCGGAAACCC
GAAAAGGCTTCTACACAGCAGCCTACTTCATCGGCCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATGGTGTGAGTCCATTGGAGAAGCTTTGGATCAGCATTGTTAAACACCAAAATCAGGAAG
GTAAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTGCTGCTTCAACAGGGTGTCAAGGATTTAAGGAA
ACCTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGCTTGTGTTATTTTAAATTT
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGGTTAAAGGTTCAACTTAAGGTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAAGATTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTAGCCTTTCAAAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGTGCGCCAGGCGCCCCGCTCTAGCTACTGTCCTGCTGCTGCTGCCAGGAGGCC
GCCATCCTGGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTTACTCACGTGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTTCCATGCTAGCGTCCCAGCTTGGCTCTGTAAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCCAATGCTATTGGTTAAAGTTGTTAATTATTGGTT
AAGATTGCTAAGGCAAAGGAAATGCGAAATCAAGTCTGTCAGTACAATAACATTGGTTAAAGAAAATGGAT
CCCACGTGTTCTCTTGCACAGAAGAACCCAGGCCACAGGCTCTGTCGCTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTTGATCAGCCTCACATGCCATT
TGTGGGGGACATTAGCAACATCACTCAGAACCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCATT
GCCGTGCTGAACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGG
GAATGGCTCTCAACTCACCTGCTTCACTGCTTCAAGTGTCTGGTTTTTAACTTGTACAGCTTTTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCTGATGGCATCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCAAGTGTAGGGTAGCCTTATTGCCCCCTTCTTCTTAAACCTTCTACACTAGTGCCTA
TGGGAACCAAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTTAGATGAATGTGACTCAAGACTCGAGGCCGATAACGGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267